STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/567,992
Source: IFWO
Date Processed by STIC: 10/23/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/567,992

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line **not exceed 72** characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — ~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 10/23/2006
PATENT APPLICATION: US/10/567,992   TIME: 17:53:58

Input Set : A:\Sequence Listing in Computer Readable Form.txt
Output Set: N:\CRF4\10232006\J567992.raw

```
     3 <110> APPLICANT: Stewart, Russell J
     4         Kiser, Patrick F
     5         Staynor, Richard S
     7 <120> TITLE OF INVENTION: Crosslinking Within Coordination Complexes
     9 <130> FILE REFERENCE: p01129-WO-00
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/567,992
C--> 11 <141> CURRENT FILING DATE: 2006-02-09
    11 <150> PRIOR APPLICATION NUMBER: 60/494,349
    12 <151> PRIOR FILING DATE: 2003-08-11
    14 <160> NUMBER OF SEQ ID NOS: 9
    16 <170> SOFTWARE: PatentIn version 3.2
```

ERRORED SEQUENCES

```
    85 <210> SEQ ID NO: 5
    86 <211> LENGTH: 10
    87 <212> TYPE: PRT
    88 <213> ORGANISM: Artificial
    90 <220> FEATURE:
    91 <223> OTHER INFORMATION: sequence for HIS-tag
    93 <220> FEATURE:
    94 <221> NAME/KEY: MISC_FEATURE
    95 <222> LOCATION: (10)..(10)
    96 <223> OTHER INFORMATION: linkage to a monomeric titin I28 Ig domain
    98 <400> SEQUENCE: 5
   100 Tyr Gly Tyr Gly His His His His His His
E-->101 1               5               10
   154 <210> SEQ ID NO: 9
   155 <211> LENGTH: 9
   156 <212> TYPE: PRT
W-->157 <213> TYPE: Artificial
E-->157 <212> TYPE: Artificial
   159 <220> FEATURE:
   160 <223> OTHER INFORMATION: sequence for HIS-tag
   162 <220> FEATURE:
   163 <221> NAME/KEY: MISC_FEATURE
   164 <222> LOCATION: (9)..(9)
   166 <213> ORGANISM:
   166 <400> SEQUENCE: 9
   168 His His His Gly Tyr Gly His His His
   169 1               5
E-->170 ??
```

(Handwritten annotations:) What is the source of genetic material? (pg.1-2) — Invalid response — Does Not Comply Corrected Diskette Needed — Pls use Numeric identifier <213> for organism — For organism response #11 = on error summary sheet! — See item <213> — Same error — delete, duplicate — OK — 10 5 10 — 5 — delete — See item #11 on = error summary sheet.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING   DATE: 10/23/2006
PATENT APPLICATION: US/10/567,992   TIME: 17:53:59

Input Set : A:\Sequence Listing in Computer Readable Form.txt
Output Set: N:\CRF4\10232006\J567992.raw

E--> 172 ??
E--> 174 ??
E--> 176 ??
E--> 178 P01129.WO.00.txt
E--> 180 Page 4

pls delete

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/23/2006
PATENT APPLICATION: US/10/567,992   TIME: 17:54:00

Input Set : **A:\Sequence Listing in Computer Readable Form.txt**
Output Set: **N:\CRF4\10232006\J567992.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8

VERIFICATION SUMMARY　　　　　　　　DATE: 10/23/2006
PATENT APPLICATION: **US/10/567,992**　　　TIME: 17:54:00

Input Set : **A:\Sequence Listing in Computer Readable Form.txt**
Output Set: **N:\CRF4\10232006\J567992.raw**

```
L:11  M:270 C: Current Application Number differs, Replaced Current Application No
L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:101 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:157 M:280 W: Numeric Identifier already exists, Type not replaced.
L:157 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:9
L:166 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:170 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:170 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:172 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:172 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:172 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=9
L:174 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:174 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:176 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:176 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:178 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:178 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:180 M:252 E: No. of Seq. differs, <211> LENGTH:Input:9 Found:10 SEQ:9
```